

Attachment #3

10/501629

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: January 15, 2008, 16:55:28 ; Search time 1 Seconds
(without alignments)
0.057 Million cell updates/sec

Title: US-10-501-629-2
Perfect score: 1209
Sequence: 1 MSKGAEFTGVVPILIELNG.....IYFEFVTAAATHGMDLYK 238

Scoring table: PAM320
Gapop 1.0 , Gapext 0.1

Searched: 1 seqs, 238 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : gfp_aeqvi.uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID		Description	
1	1179	97.5	238	1	GFP_AEQVI	Green fluorescent	

ALIGNMENTS

RESULT 1

GFP_AEQVI

ID GFP_AEQVI STANDARD; PRT; 238 AA.
AC P42212; Q17104; Q27903;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 25-JUL-2006, entry version 56.
DE Green fluorescent protein.
GN Name=GFP;
OS Aequorea victoria (Jellyfish).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;

Parameters used

Scoring matrix -
Pam 320

gap penalty 1

gap size penalty 0.1

OC Aequoreidae; Aequorea.
 OX NCBI_TaxID=6100;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=92175527; PubMed=1347277; DOI=10.1016/0378-1119(92)90691-H;
 RA Prasher D.C., Eckenrode V.K., Ward W.W., Prendergast F.G.,
 RA Cormier M.J.;
 RT "Primary structure of the Aequorea victoria green-fluorescent
 RT protein.";
 RL Gene 111:229-233(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=94185810; PubMed=8137953; DOI=10.1016/0014-5793(94)80472-9;
 RA Inouye S., Tsuji F.I.;
 RT "Aequorea green fluorescent protein. Expression of the gene and
 RT fluorescence characteristics of the recombinant protein.";
 RL FEBS Lett. 341:277-280(1994).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=97299832; PubMed=9154981; DOI=10.1023/A:1005740823703;
 RA Rouwendal G.J.A., Mendes O., Wolbert E.J.H., de Boer A.D.;
 RT "Enhanced expression in tobacco of the gene encoding green fluorescent
 RT protein by modification of its codon usage.";
 RL Plant Mol. Biol. 33:989-999(1997).
 RN [4]
 RP CHROMOPHORE.
 RX MEDLINE=93192221; PubMed=8448132;
 RA Cody C.W., Prasher D.C., Westler W.M., Prendergast F.G., Ward W.W.;
 RT "Chemical structure of the hexapeptide chromophore of the Aequorea
 RT green-fluorescent protein.";
 RL Biochemistry 32:1212-1218(1993).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=96355665; PubMed=8703075;
 RA Ormoe M., Cubitt A.B., Kallio K., Gross L.A., Tsien R.Y.,
 RA Remington S.J.;
 RT "Crystal structure of the Aequorea victoria green fluorescent
 RT protein.";
 RL Science 273:1392-1395(1996).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=98294543; PubMed=9631087; DOI=10.1038/nbt1096-1246;
 RA Yang F., Moss L.G., Phillips G.N. Jr.;
 RT "The molecular structure of green fluorescent protein.";
 RL Nat. Biotechnol. 14:1246-1251(1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW EMISSION.
 RX MEDLINE=98455509; PubMed=9782051; DOI=10.1016/S0969-2126(98)00127-0;
 RA Wachter R.M., Elsliger M.A., Kallio K., Hanson G.T., Remington S.J.;
 RT "Structural basis of spectral shifts in the yellow-emission variants
 RT of green fluorescent protein.";
 RL Structure 6:1267-1277(1998).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=99238303; PubMed=10220315; DOI=10.1021/bi9902182;
 RA Elsliger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
 RT "Structural and spectral response of green fluorescent protein

RT variants to changes in pH.";

RL Biochemistry 38:5296-5301(1999).

CC -!- FUNCTION: Energy-transfer acceptor. Its role is to transduce the
 CC blue chemiluminescence of the protein aequorin into green
 CC fluorescent light by energy transfer. Fluoresces in vivo upon
 CC receiving energy from the Ca(2+)-activated photoprotein aequorin.

CC -!- BIOPHYSICOCHEMICAL PROPERTIES:

CC Absorption:

CC Abs(max)=395 nm;

CC Note=Exhibits a smaller absorbance peak at 470 nm. The
 CC fluorescence emission spectrum peaks at 509 nm with a shoulder
 CC at 540 nm;

CC -!- SUBUNIT: Monomer.

CC -!- TISSUE SPECIFICITY: Photocytes.

CC -!- PTM: Contains a chromophore consisting of modified amino acid
 CC residues. The chromophore is formed by autocatalytic backbone
 CC condensation between Xaa-N and Gly-(N+2), and oxidation of Tyr-
 CC (N+1) to didehydrotyrosine. Maturation of the chromophore requires
 CC nothing other than molecular oxygen.

CC -!- BIOTECHNOLOGY: Fluorescent proteins have become a useful and
 CC ubiquitous tool for making chimeric proteins, where they function
 CC as a fluorescent protein tag. Typically they tolerate N- and C-
 CC terminal fusion to a broad variety of proteins. They have been
 CC expressed in most known cell types and are used as a noninvasive
 CC fluorescent marker in living cells and organisms. They enable a
 CC wide range of applications where they have functioned as a cell
 CC lineage tracer, reporter of gene expression, or as a measure of
 CC protein-protein interactions.

CC -!- SIMILARITY: Belongs to the GFP family.

CC -!- WEB RESOURCE: NAME=Protein Spotlight; NOTE=Issue 11 of June 2001;
 CC URL="http://www.expasy.org/spotlight/back_issues/sptlt011.shtml".

CC -----

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 CC -----

DR EMBL; M62654; AAA27722.1; -; mRNA.

DR EMBL; M62653; AAA27721.1; -; mRNA.

DR EMBL; L29345; AAA58246.1; -; mRNA.

DR EMBL; X96418; CAA65278.1; -; mRNA.

DR PIR; JS0692; JQ1514.

DR PDB; 1B9C; X-ray; A/B/C/D=2-238.

DR PDB; 1BFP; X-ray; @=1-238.

DR PDB; 1C4F; X-ray; A=1-238.

DR PDB; 1CV7; X-ray; A=-.

DR PDB; 1EMA; X-ray; @=1-238.

DR PDB; 1EMB; X-ray; @=1-238.

DR PDB; 1EMC; X-ray; A/B/C/D=2-237.

DR PDB; 1EME; X-ray; @=2-237.

DR PDB; 1EMF; X-ray; @=2-238.

DR PDB; 1EMG; X-ray; A=1-238.

DR PDB; 1EMK; X-ray; @=2-237.

DR PDB; 1EML; X-ray; @=2-237.

DR PDB; 1EMM; X-ray; @=2-238.

DR PDB; 1F09; X-ray; A=1-238.

DR PDB; 1F0B; X-ray; A=1-238.

DR PDB; 1GFL; X-ray; A/B=2-238.

DR PDB; 1H6R; X-ray; A/B/C=-.

DR PDB; 1HCJ; X-ray; A/B/C/D=1-238.
 DR PDB; 1HUY; X-ray; A=2-238.
 DR PDB; 1JBY; X-ray; A=1-238.
 DR PDB; 1JBZ; X-ray; A=1-238.
 DR PDB; 1JC0; X-ray; A/B/C=1-238.
 DR PDB; 1JC1; X-ray; A/B/C=1-238.
 DR PDB; 1KP5; X-ray; A/B=3-238.
 DR PDB; 1KYP; X-ray; A=-.
 DR PDB; 1KYR; X-ray; A=-.
 DR PDB; 1KYS; X-ray; A=-.
 DR PDB; 1MYW; X-ray; A=-.
 DR PDB; 1Q4A; X-ray; A=1-238.
 DR PDB; 1Q4B; X-ray; A=1-238.
 DR PDB; 1Q4C; X-ray; A=1-238.
 DR PDB; 1Q4D; X-ray; A=1-238.
 DR PDB; 1Q4E; X-ray; A=1-238.
 DR PDB; 1Q73; X-ray; A=1-238.
 DR PDB; 1QXT; X-ray; A=2-229.
 DR PDB; 1QY3; X-ray; A=1-229.
 DR PDB; 1QYF; X-ray; A=2-229.
 DR PDB; 1QYO; X-ray; A=2-238.
 DR PDB; 1QYQ; X-ray; A=-.
 DR PDB; 1RM9; X-ray; A=2-238.
 DR PDB; 1RMM; X-ray; A=2-229.
 DR PDB; 1RMO; X-ray; A=2-238.
 DR PDB; 1RMP; X-ray; A=2-229.
 DR PDB; 1RRX; X-ray; A=2-229.
 DR PDB; 1W7S; X-ray; A/B/C/D=1-238.
 DR PDB; 1W7T; X-ray; A/B/C/D=1-238.
 DR PDB; 1W7U; X-ray; A/B/C/D=1-238.
 DR PDB; 1YFP; X-ray; A/B=3-229.
 DR PDB; 1YHG; X-ray; A/B=2-238.
 DR PDB; 1YHH; X-ray; A=2-238.
 DR PDB; 1YHI; X-ray; A=2-238.
 DR PDB; 1YJ2; X-ray; A=-.
 DR PDB; 1YJF; X-ray; A=-.
 DR PDB; 1Z1P; X-ray; A=-.
 DR PDB; 1Z1Q; X-ray; A=-.
 DR PDB; 2AH8; X-ray; A/B=-.
 DR PDB; 2AHA; X-ray; A/B=-.
 DR PDB; 2AWJ; X-ray; A=2-229.
 DR PDB; 2AWK; X-ray; A=2-229.
 DR PDB; 2AWL; X-ray; A=2-229.
 DR PDB; 2AWM; X-ray; A=2-229.
 DR PDB; 2B3Q; X-ray; A/B/C/D=1-238.
 DR PDB; 2EMD; X-ray; @=2-238.
 DR PDB; 2EMN; X-ray; @=2-238.
 DR PDB; 2EMO; X-ray; @=2-238.
 DR PDB; 2FWQ; X-ray; A=-.
 DR PDB; 2FZU; X-ray; A=-.
 DR PDB; 2G16; X-ray; A=-.
 DR PDB; 2G2S; X-ray; B=-.
 DR PDB; 2G3D; X-ray; B=66-238.
 DR PDB; 2G5Z; X-ray; A=2-64, B=-.
 DR PDB; 2G6E; X-ray; A=-.
 DR LinkHub; P42212; -.
 DR GO; GO:0008218; P:bioluminescence; TAS.

DR GO; GO:0006091; P:generation of precursor metabolites and energy; TAS.
 DR InterPro; IPR009017; GFP_like.
 DR InterPro; IPR011584; GFP_related.
 DR InterPro; IPR000786; Green_fl_protein.
 DR Pfam; PF01353; GFP; 1.
 DR PRINTS; PR01229; GFLUORESCENT.
 DR ProDom; PD013756; Green_fl_protein; 1.
 KW 3D-structure; Chromophore; Direct protein sequencing; Luminescence;
 KW Photoprotein.
 FT CHAIN 1 238 Green fluorescent protein.
 FT /FTId=PRO_0000192576.
 FT MOD_RES 66 66 (Z)-2,3-didehydrotyrosine.
 FT CROSSLNK 65 67 5-imidazolinone (Ser-Gly).
 FT VARIANT 100 100 F -> Y.
 FT VARIANT 108 108 T -> S.
 FT VARIANT 141 141 L -> M.
 FT VARIANT 219 219 V -> I.
 FT CONFLICT 2 2 S -> G (in Ref. 3).
 FT CONFLICT 25 25 H -> Q (in Ref. 2).
 FT CONFLICT 80 80 Q -> R (in Ref. 3).

Query Match 97.5%; Score 1179; DB 1; Length 238;
 Best Local Similarity 92.9%; Pred. No. 0;
 Matches 221; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 MSKGAELFTGVVPILIELNGDVNGHKFSVSGEGEDATYGKLTCLKFICTTGKLPVPWPPTL 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEDATYGKLTCLKFICTTGKLPVPWPPTL 60

Qy     61 VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYIQERTIFFKDDGNYKSRAEVKFEGDTLV 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 VTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 120

Qy    121 NRIELTGTDFKEDGNILGNKMEYNYNAHNVIIMTDKAKNGIKVNFKIRHNIEDGSVQLAD 180
      ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 NRIELKGIDFKEDGNILGHKLEYNNSHNVIIMADKQKNGIKVNFKIRHNIEDGSVQLAD 180

Qy    181 HYQQNTPIGDGPVLLPDNHYLSTQSTLSKDPNEKRDHMIYFEFVTAAGITHGMDELYK 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 HYQQNTPIGDGPVLLPDNHYLSTQSALS KDPNEKRDHMLLEFVTAAGITHGMDELYK 238

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Search completed: January 15, 2008, 16:55:29
 Job time : 2 secs